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Listing first 45 summaries
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245
1 SQRQFQECQQHCHQOEORPF.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 2
VCLA_GOSHI
ID VCLA_GOSHI

STANDARD;

PRT;

605 AA.

рb

Query Match 94.3%; Score 231; DB 1; Length 588; Best Local Similarity 92.9%; Pred. No. 5.9e-18; Matches 39; Conservative 2; Mismatches 1; Indels

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M16891; AAA33071.1; A30838; FWCNAB. P50477; 1CAX. PF00546; Seedstore_7s; 1. storage protein; Signal. L 1 25 L 2 588 VICILIN C72. NCE 588 AA; 69729 MW; 63E699B29AB	CONVICILIN, CONGLYCININ, ETC.). s SWISS-PROT entry is copyright. It is ween the Swiss Institute of Bioinfor European Bioinformatics Institute. by non-profit institutions as lon ified and this statement is not removities requires a license agreement (seend an email to license@isb-sib.ch).	UENCE FROM N.A. an C.A., Pyle J.B., Legocki A.B., Du an C.A., Pyle J.B., Legocki A.B., Du an C.A., Pyle J.B., Legocki A.B., Du wellopmental biochemistry of cottonse mination. XVIII. cDNA and amino acid storage protein families."; storage protein families."; nt Mol. Biol. 7:475-489(1986). FUNCTION: SEED STORAGE PROTEIN. SUBCELLULAR LOCATION: COTYLEDONARY BODIES. SUMILARITY: TO OTHER 75 SEED STORAGE STORAGE PROTEIN.	B_GOSHI STANDARD; PRT; 58 BO1; MAR-1989 (Rel. 10, Created) MAR-1989 (Rel. 10, Last sequence upo JUL-1999 (Rel. 38, Last annotation upo ILIN C72 PRECURSOR (ALPHA-GLOBULIN upo Syplum hirsutum (Upland cotton). aryota; Viridiplantae; Embryophyta; nollophyta; eudicotyledons; core eudvales; Malvaceae; Gossypium.	ALIGNMENTS	58.5 23.9 450 1 SRE_DROME 58.5 23.9 1541 1 YHY6_YEAST 58 23.7 395 1 SRY_MOUSE 58 23.7 395 1 SRY_MOUSE 58 23.7 429 1 APA4_MACFA 58 23.7 594 1 RBJK_DROME 58 23.7 678 1 DORS_DROME 58 23.7 832 1 YFC4_YEAST 58 23.7 864 1 E78A_DROME 58 23.7 1023 1 CLOC_DROME 58 23.7 1784 2 TRHY_SHEEP 58 23.7 1784 1 INVO_HUMAN
CRC64;	roduced through a coll ics and the EMBL out re are no restriction as its content is in Usage by and for c http://www.isb-sib.ch/	TITE L. III; Led embryogenesis and Led sequences of the members of MEMBRANE-BOUND VACUOLAR PROTEIN MEMBRANE-BOUND VACUOLAR PROTEIN	AAA. Jate) ppdate) 3). Tracheophyta; Spermatophyta; Jicots; Rosidae; eurosids II;	, ,	Q24535 drosophila P38873 saccharomyc Q05738 mus musculu P33621 macaca fasc P28159 drosophila P15330 drosophila P43572 saccharomyc P45447 drosophila O61735 drosophila P22793 ovis aries P07207 drosophila P07476 homo sapien

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TRX_DROVI
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Best Local S
Matches 30
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Q24742;
Q1-OCT-2000
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TRITHORAX PR
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Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Pterygota; Nrosophilidae; Drosophila.
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01-MAR-1989
01-MAR-1989
15-JUL-1999
                                                                        "Conservation of structure and expression between Drosophila virilis and Drosophila Mech. Dev. 53:113-122(1995).
                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=96100387; PubMed=8555104;
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"Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the globulin (vicilin) genes of cottonseed.";
Plant Mol. Biol. 9:533-546(1987).
-!- FUNCTION: SEED STORAGE PROTEIN.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Sj
Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
                                                                                                                                                         Tillib S., Sedkov Y., Mizrokhi
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FUNCTION: FUNCTIONS IN SEGMENT DETERMINATION THROUGH INTERACTION WITH GENES OF BITHORAX (BX-C) AND ANTENNAPEDIA (ANT-X) COMPLEXES IT CAN BEHAVE AS AN ACTIVATOR OF BX-C.
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RESULT 4
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MEDLINE-89030681; PubMed-3181153; Menendez-Arias L., Moneo I., Dominguez J., Further and Structure of the major allergen of alba L.) seed, Sin a I."; Eur. J. Biochem. 177:159-166(1988).
                                                                                                                            ALL1_SINAL STANDARD; PRT; 127 AA. P15322; 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) ALLERGEN SIN A 1, SMALL AND LARGE CHAINS (SIN A 1).
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DOMAIN
                                                                                              Sinapis alba (White mustard) (Brassica hirta).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosida
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                                                                                       Brassicales; Brassicaceae; Sinapis.
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                       (Sinapis
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В
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ALL1_BRAJU
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Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last annotation update)
ALLERGEN BRA J 1-E, SMALL AND LARGE CHAIRD.
Brasslca juncea (Leaf mustard) (Indian mustard).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Buharyota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brasslcalco Brasslcalco Control endicots; Rosidae; eurosids II;
Brasslcalco Brasslcalco Control endicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALL1_BRAJU STANDARD;
P80207; P80215;
01-OCT-1993 (Rel. 27, Created)
                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1993 (Rel. 27, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation updat ALLERGEN BRA J 1-E, SMALL AND LARGE CHAINS
                                                                                                                                                                                                                                                                 allergen, Bra j IE: detection of an allergenic Biochem. J. 293:625-632(1993).
                                                                                                                 VARIANT
                                                                                                                            VARIANT
                                                                                                                                                   NON_CONS
                                                                                                                                                                      Allergen;
                                                                                                                                                                                                                   LINKED BY TWO DISULFIDE BONDS.
                                                                                                                                                                                                                                       -!- FUNCTION: THIS IS A 2S SEED STORAGE PROTEIN.
                                                                                                                                                                                                                                                                                                   Monsalve R.I., Gonzalez de la Pena M.A.,
Lopez-Otin C., Villalba M., Rodriguez R.;
                                                                                                                                                                                                                                                                                                                         MEDLINE=93356721; PubMed=7688955;
                                                                                                                                                                                                                                                                                                                                        TISSUE=SEED;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          Brassicales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF01631; Seedstore_2S; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S01792; S01792
PIR; S01791; S01791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DISEASE: ALLERGIC DISEASE, -!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                            INTERPRO;
                                                                                                                                                                                                                                                                                      "Characterization of a new oriental-mustard (Brassica juncea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION:
 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 RKEFQQAQHLRACQQWLHKQAMQSGSGPSPQGPQQRPPLLQQC---CNELHQEEP 62
                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QRQFQE-----CQQHCHQQ------EQRPEKKQQCVRECREKYQENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BONDS
                      QRQFQE----CQQHCHQQ--
RKEFQQAQHLRACQQWLHKQAMQSGSGPQPQGPQQRPPLLQQC---CNELHQEEP 61
                                                                                                                                                                                           PF01631; Seedstore_2S; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                   PR00496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR00496; NAPIN
                                                                                                                                                                                                          IPR000617;
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1 39 SM
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                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Brassicaceae; Brassica.
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40
                                                                                                                                                               1 storage
1 37
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THE PROTEIN CONSISTS OF TWO CHAINS
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32.7%;
                                                        32
32
                                                                                                                                                                      protein
                                                                    .0%;
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                                                                                                             LARGE CHAIN.
F -> I.
R -> K.
                                                      Score
Pred.
                    -----EQRPEKKQQCVRECREKYQENP 37
                                                                                                                                                            SMALL CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 71; DB 1
Pred. No. 0.21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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2S SEED STORAGE ALBUMINS
                                                                                                     D6F28E03F62B08F8 CRC64;
                                             Mismatches
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No.
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0.21;
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                                                                 Length 129
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RESULT 7
LP61_EIMTE
ID LP61_EIMTE
AC P15714;
DT 01-APR-1990
     RC OCC
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Best Local S
Matches 18
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P38057;
01-OCT-1994
01-OCT-1994
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Last sequence up of the control of the contr
                                                                                                              Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                               Eimeria tenella
                                                                                                                                                                    01-APR-1990 (Rel.
01-FEB-1994 (Rel.
ANTIGEN LPMC-61 (F
                                                                                                                                                                                                     01-APR-1990
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L), a member of the napin protein family.";
Int. J. Pept. Protein Res. 43:425-430(1994).
-i- FUNCTION: INHIBITS TRYPSIN WITH A KI OF 7 X
-i- SUBUNIT: THE PROTEIN CONSISTS OF TWO CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Svendsen I.B., Nicolova D., Goshev I., Genov N.; "Primary structure, spectroscopic and inhibitory potanin trypsin inhibitor from the seeds of charlock
                                                                                      Eimeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seed storage
CHAIN
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TISSUE=SPOROZOITE;
                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94350545; PubMed=8070965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKEFQQAQHLRACQQWLHKQARQSGSGPSPQGPQQRPPLLQQC---CNELHQEEP
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                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                       (FRAGMENT)
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                                                                                                                                                                                         14, Created)14, Last sequence update)28, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14682 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71; DB
Pred. No. 0.21
7; Mismatches
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A - > M.

B - M.
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0.21;
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ck (Sinapis
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RESULT 8
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Best Local
Banri S., Servadio A., Chung M.-Y., Kwiatkowski T.J. Jr., McCall Duvick L.A., Shen Y., Roth E.J., Orr H.T., Zoghbi H.Y.; "Identification and characterization of the gene causing type 1 spinocerebellar ataxia.";
                                             TISSUE=CEREBELLUM, AND BRAIN; MEDLINE=95038838; PubMed=7951322;
                                                                                                   Eukaryota;
                                                                                                                                    ATAXIN-1 (SPINOCEREBELLAR ATAXIA
                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                   P54253;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen;
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification and characterization of a target antigen of a monocolonal antibody directed against Eimeria tenella merozoites."; Mol. Biochem. Parasitol. 41:53-64(1990).
                                                                    SEQUENCE FROM N.A.
                                                                                         Mammalia;
                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                         ATX1_HUMAN
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                                                                                                                                                                                                                                                                  1 SQRQFQECQQHCHQQ-----EQRPEKKQQCVRECREKYQENPW 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: MAY BE COVALENTLY LINKED BY DISPOSITEDES TO FORM THE 80 KDA ANTIGEN DEVELOPMENTAL STAGE: PRESENT IN ALL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: UNKNOWN. THE GLN-RICH TANDEM REPEATS MAY BE IMPORTANT FOR AN UNKNOWN ASPECT OF THE PARASITIC LIFE CYCLE. MAY BE AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXCYSTATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT IMMUNOGEN
                                                                                                                                                                                                                                           A60637; A60637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith C.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sporozoite; Repeat;
                                                                                        Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                              255 AA;
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49
58
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                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II, McDonell M.;
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152
172
192
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                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                    TYPE
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                                                                                                                                  update)
1 PROTEIN)
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RESULT 9
YAK1_YEAST
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Best Local
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P14680;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence upda
01-OCT-2000 (Rel. 40, Last annotation uf
PROTEIN KINASE YAKI (EC 2.7.1.-).
YAKI OR YJL141C OR J0652.
YAKI OR YJL141C OR J0652.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-90108683; PubMed-2558053;

Garrett S., Broach J.;

"Loss of Ras activity in Saccharomyces cerevisiae is suppressed disruptions of a new Kinase gene, YAKI, whose product may act downstream of the cAMP-dependent protein kinase.";

Genes Dev. 3:1336-1348(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
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11- ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS ARE PRODUCED ALTERNATIVE SPLICING.

11- TISSUE SPECIFICITY: WIDELY EXPRESSED THROUGHOUT THE BOLY-GLY REGION OF SCA1 IS HIGHLY POLY-GLY REGION P
Yeast 12:787-
-i- FUNCTION:
                                                   including homologues of
chromosome XI.";
                                                                                                          chromosome X reveals
                                                                                                                                                                                    STRAIN=S288C / FY1679;
MEDLINE=96408771; PubMed=8813765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                          Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.; "Sequence analysis of a 40.7 kb segment from the left arm of yeast chromosome x reveals 14 known genes and 13 new open reading frames including homologues of genes clustered on the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
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DISEASE
TYPE 1; ALSO KNOWN AS OLIVOPONTOCEREBELLAR ATROPHY I (OPCA I).
SCA1 IS AN AUTOSOMAL DOMINANT NEURODEGENERATIVE DISORDER
CHARACTERIZED BY PROGRESSIVE NEURONAL LOSS IN THE CEREBELLUM,
BRAIN STEM AND SPINOCEREBELLAR TRACTS. CLINICAL FEATURES ARE
CEREBELLAR ATAXIA, DYSARTHRIA, OPHTALMOPARESIS, MUSCLE WASTING AND
NEUROPATHY. ONSET OF THE DISEASE USUALLY OCCURS IN THE THIRD OR
FOURTH DECADE OF LIFE AND DEATH OCCURS TEN TO TWENTY YEARS LATER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (9 TO 39 REPEATS) IN THE NORMAL POPULATION AND IS EXPANDED TO ABOUT 40-81 REPEATS IN SCA1 PATIENTS. LONGER EXPANSIONS RESULT IN EARLIER ONSET AND MORE SEVERE CLINICAL MANIFESTATIONS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164400; -
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                         12:787-797(1996)
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12; Conser
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PROTEIN OCCURS

IN REVERTANT RAS/CAMP MUTANTS

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Best Local S
Matches 16
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EMBL; X87371; CAA60814.1; -.
EMBL; Z49417; CAA69437.1; -.
PIR; A32582; A32582.
HSSP; P24941; 1AQ1.
SGD; S0003677; YAK1.
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375
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01-MAR-1989
01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica napus (Rape).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MG-1992 (Rel. 23, Last annotation update)
NAPIN EMBRYO SPECIFIC PRECURSOR (1.7S SEED STORAGE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRANA
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               MEDLINE=87308225; PubMed=3040733;
Scofield S.R., Crouch M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPRO00719; -.
INTERPRO; IPRO02290; -.
PFAM; PF00069; pkinase; 2.
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                                                                                                                                                                                                                                                                                             "Nucleotide sequence of a member of the napin storage protein family
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LINKED BY DISULFIDE BONDS.
TISSUE SPECIFICITY: COTYLE
DEVELOPMENTAL STAGE: EMBRY
                                                                                               ITS MATURATION.
SUBUNIT: THE MATURE PROTEIN CONSISTS OF
                                                                                                                                                               FUNCTION: THE SMALL, BASIC, WATER-SO TWO MAJOR KINDS OF STORAGE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNB/DYRK SUBFAMILY.
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                                                                                                                                                                                                                         Brassica napus.";
iol. Chem. 262:12202-12208(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQRSPQQQHQNHHQQQQQQQQQQQQQQQQSQFCF----VNPWNEEK 96
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Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.3%;
                                     COTYLEDONS AND THE AXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E0B7C56FAA35E056 CRC64;
                                                                                                                                                                                                 WATER-SOLUBLE NAPINS
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                                                                                               A LARGE CHAIN
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RESULT 11
HOG1_HORVU
ID HOG1_H
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                       modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                "A gamma-hordein gene.";

Plant Mol. Biol. 11:449-461(1988).

Plant Mol. Biol. 11:449-461(1988).

Plant Mol. Biol. 11:449-461(1988).

Plant Mol. Biol. 11:49-461(1988).

Plant Mol. Biol. 11:449-461(1988).

Protein Molies

(AS PROTEIN BODIES).

PROTEIN BODIES).

PROTEIN BODIES).

PROTEIN BODIES).

PROTEIN BODIES AN N-TERMINAL HALF

COMPOSED OF PROLINE-GLUTAMINE BLOCKS ORGANIZED IN REPEATING UNITS

AND A C-TERMINAL HALF WHERE THE REPEATS ARE DISPERSED AND LESS
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence up
01-OCT-1996 (Rel. 34, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
SEQUENCE
EMBL; X13508; CAA31861.1;
                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                     GAMMA-HORDEIN 1 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOG1_HORVU
P17990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                 Cameron-Mills V., Brandt A.;
                                                                                                                                                                                                                                                                                                                   STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                          Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
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    -!- SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY.

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                                                                                                                                                     CONSERVED.
SIMILARITY: TO GAMMA-GLIADIN FROM WHEAT, AND A GAMMA-SECALIN FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaborate the Swiss Institute of Bioinformatics and the EMBL outstat. European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C---CNELHQEEP
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                                                                                                                                          AND LESS TO
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                                                                                                                                                                                                                                                                                                                CARINA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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76
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21013 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.18;
24.78;
                                                                                                                                         A B1 HORDEIN FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update)
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Pred.
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; 9CAE63D84B160AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                                                          Poaceae; Hordeum.
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                                        (See http://www.isb-sib.ch/announce,
                                                                                                                                         BARLEY.
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RESULT 12
SNF5_YEAST
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Best Local S
Matches 16
EMBL; M36482; AAA35062.1; EMBL; X76053; CAA53652.1; EMBL; X76053; CAA85254.1; EMBL; 236158; CAA85254.1; PIR; S44551; RGBYS5. PIR; S39145; S39145.
                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                     MEDLINE-94378722; PubMed-8091861;
Holmstroem K., Brandt T., Kallesoe T.;
"The sequence of a 32,420 bp segment located on the right arm
chromosome II from Saccharomyces cerevisiae.";
Yeast 10:S47-S62(1994).
                                                                                     or send an
                                                                                                                  modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR001954; -. PFAM; PF00279; LTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       broad spectrum of genes.";
Mol. Cell. Biol. 10:5616-5625(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proline-rich transcriptional activator that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P18480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-MCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91042489; PubMed=2233708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TRANSCRIPTION FACTOR TYE4).
SNF5 OR TYE4 OR SWI10 OR YBR289W OR YBR2036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaurent B.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
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nes 16; Conserv
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                                                                                 ween the Swiss Institute of Bioinformat
European Bioinformatics Institute. The
by non-profit institutions as long
ified and this statement is not removed.
ities requires a license agreement (See
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.
SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                                                    SUBCELLULAR LOCATION: SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                       FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION.
COMPLEX IS REQUIRED FOR THE INDICED EXPRESSION OF
                                                                                                                                                                                                                                    COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNF5 protein of Saccharomyces cerevisiae is a gine-rich transcriptional activator that affects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S08312; S08312.
RPRO; IPR000528; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            storage protein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQQQFPQPPQQPFPQQPQPFPQSQQQCLQQPQHQFPQPTQQFPQR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 м36378;
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305 AA;
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                                          AAA35062.1; -. CAA53652.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treitel M.A., Carlson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA32955.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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34737 MW;
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35.6%;
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                                                                                                                                                                                                      NUCLEAR.
O THE SNF5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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2; Mismatches
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                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
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                                                                                                                Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                a glutamine- and cts expression of
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                                                                                                                                                       EMBL outstation
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Best Local S
Matches 12
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Q07283;
Q1-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                envelope precursor, and an intermedia linking) protein.";
J. Biol. Chem. 268:12164-12176(1993).
                                                                                                                                                                                                                                                                                                                                                                            O'Keefe E.J., Hamilton E.H., Lee S.-C., "Trichohyalin: a structural protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994 (Rel.
01-OCT-1994 (Rel.
01-OCT-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                J. Invest. Dermatol. 101:65S-71S(1993).
                                                                                                                                                                                                                                                                                                                                                              epidermis."
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93315897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93280194; PubMed=7685034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THH OR TRHY OR THL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRICHOHYALIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1731-1898 FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                functional EF-hand-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steinert P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee S.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The structure of human trichohyalin. Potential multiple roles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                           SUBUNIT: MONOMER (PROBABLE).
TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SUTTED INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AND THE FILLFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE).
DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF
             DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INVERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAIN 6 DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN
                                                                                                                                                                                                                      FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CALL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CALL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CALL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN THE KIF NETWORK.
                                                                                                                     THE EPIDERMIS
                                                                                                                                                                                                             DIFFERENTIATION.
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12; Conserv
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905
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324
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882
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102557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30, Created)
30, Last sequal 40, Last annotation
 DOMAIN 9 CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=7686953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
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PRO-RICH.
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A287B4A648DD1A35 CRC64;
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No.
THE C-TERMINUS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0'Keefe
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                                                                                                                                                                                                                                                                                                                                                                          hair, tongue, nail,
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5.7;
                                                                                                                                                                                                                                                                                                                                                                                          Steinert P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein, a cornified cell
filament-associated (cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                         DOMAIN
CONFLICT
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REPEAT
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                                                                                                                                                                                    REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00018; EF_HAND; 1. PROSITE; PS00303; S100_CABP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPR001751; -.
INTERPRO; IPR002048; -.
PFAM; PF01023; S_100; 1.
PFAM; PF00036; efhand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02633
MIM; 190370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L09190; AAA65582.1; PIR; A45973; A45973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
                  2 QRQFQECQQHCHQQEQRPEKKQQCVRECREKYQ----ENPWRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIFFERENT SPECIES PTM: KNOWN SUBSTR.
KRRRQERERQCREEEELQQEEEQLLREEREKRRRQELERQYREE
                                                                                                                                                                                                                                                                                                                                                                                                                ; PS00303; Sac
;; Calcium-binding.
; 21 91
3 22 33
73
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                                     l Similarity
14; Conser
                                                                                    983
1013
1043
1073
11073
11133
1155
1752
1752
1794
1857
1880
1880
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391
397
403
409
415
421
421
                                      Conservative
                                                                             1880
9 AA;
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702
1162
952
                                                                                                      982
1012
1042
1042
1072
1102
11132
11162
11162
11849
1752
1869
1875
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377
390
444
402
402
414
420
432
438
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339
351
                                                                                                                                                                                                                                                                                                                                                                                                           390
                                               26.1%;
                                                                                    247219
                                              .88
                                                                                 23 X 26 AA APPROXIMATE
F -> L (IN REF. 2).
QERDRQYR -> RSETGSTG (
Q -> K (IN REF. 2).
V -> G (IN REF. 2).
9 MW; A74B5947FB62E31D C
                                     14;
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8 X

8 X

4-1

4-2

4-5

4-5
                                    Pred. No. 13;
4; Mismatches
                                                       Score
                                                                                                                                            4-8
                                                                                                                                                                                                                                                                                                                                                                                      6 X 13 AA TANDEM REPEATS OF R-R-E-Q-E-E-E-R-R-E-Q-Q-L.
1-1 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                   SITE I (LOW AFFINITY) (POTENTIAL)
SITE II (HIGH AFFINITY) (POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                       S-100 LIKE
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30
                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                     (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                              (APPROXIMATE).
                                             No.
                                                                                                                                                                                                                                                                                                                               ΑA
                                                                                                             5 AA APPROXIMATE TANDEM REPEATS (IN REF. 2).
YR -> RSETGSTG (IN REF. 2).
                                                                                                                                                                                                                       AA TANDEM REPEATS.
                                           DB
. 13;
                                                                                                                                                                                                                                                                                                                               TANDEM
                                    12;
                                                                                                                                                                                                                                                                                                                               REPEATS
                                                      Length 1898;
1160
                  41
                                                                                                                                                                                                                                                                                                                              G,
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              R-R-E-Q-Q-L
                                    4;
                                    Gaps
                                   1:
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RESULT 15
2SS2_BRANA STANI
ID 2SS2_BRANA STANI
AC P01090;
DT 21-JUL-1986 (Rel. 0;
DT 01-MAR-1989 (Rel. 1;
DT 01-AUG-1992 (Rel. 2;
DE NAPIN 2 PRECURSOR (;
OS Brassica napus (Rapo
C Eukaryota; Viridipli
OC Magnoliophyta; eudi;
OC Brassicales; Brassicales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14

2SSI_BRANA
AC 24565;
AC P24565;
DT 01-MAR-1992 (
DE WASIGNAL -92111
RA MADINE-92111
RA MEDLINE-92111
RA MEDLINE-92111
RA MEDLINE-92111
RA MEDLINE-92111
RA MEDLINE-92111
RA MEDLINE-92111
RA MEDUNIT:
CC -!- WISCELLAN
CC -!- WISCELLAN
CC -!- MISCELLAN
CC -!- MISCELLAN
CC -!- MISCELLAN
CC -!- MISCELLAN
CC -!- SIMILARIT
CC -!- SIMILARIT
DR PIN; S20350;
DR INTERPRO; IPR
DR PIN; S20350;
DR INTERPRO; IPR
DR PIN; S20350;
DR INTERPRO; IPR
DR PIN; S20350;
DR VARIANT
FT VARIANT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                       Brassica napus (Rape).
Brassica napus (Rape).
Eukaryota; Viridiplantae; Embryophyta;
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core euc
Magnoliophyta; Rrassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
NAPIN 2 PRECURSOR (1.78 SEED STORAGE PROTEIN)
                                                           "Structure of a gene end
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Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core eu
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01-MAR-1992 (Rel. 21, Last sequence up
01-MAR-1992 (Rel. 21, Last annotation
NAPIN IA AND IB SMALL CHAIN AND LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: THE SMALL, BASIC, WATER-SOLUBLE NAPINS ARE ONE OF TWO MAJOR KINDS OF STORAGE PROTEINS SYNTHESIZED IN THE SEED ITS MATURATION.

-i- SUBBOLIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND A LARGE
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MEDLINE=92111741; PubMed=1765156;
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-!- SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANEOUS:
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                                                     A. PubMed=3624251; Thoman M., Ericson M.L. Thoman M., Ericson M.L. The 1.7 s
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E -> Q (IN NAPIN IB).
MISSING (IN NAPIN IB).
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RA Crouch M.L., Tenbarge K.M., Simon A.E., Ferl R.;

RA Crouch M.L., Tenbarge K.M., Simon A.E., Ferl R.;

RA Crouch M.L., Tenbarge K.M., Simon A.E., Ferl R.;

RT nucleotide sequence analysis that both subunits of napin are cleaved from a precursor polypeptide.";

RL J. Mol. Appl. Genet. 2:273-283(1983).

CC -i- FUNCTION: THE SMALL, BASIC, WATER-SOLUBLE NAPINS ARE ONE OF THE CC TWO MAJOR KINDS OF STORAGE PROTEINS SYNTHESIZED IN THE SEED DURING CC ITS MATURATION.

CC -I- SUBUNIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND A LARGE CHAIN CC -I- SUBUNIT: THE MATURE PROTEIN CONSISTS OF A SMALL AND A LARGE CHAIN CC -I- SIMILARITY: BELONGS TO THE 2S SEED STORAGE ALBUMINS FAMILY.
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                         PFAM; PF01631; Seedstore_2S; 1.

PRINTS; PR00A96; NAPIN.

Seed storage protein; Signal; Multigene family.

SIGNAL 1 21
PROPEP 2 38
CHAIN 39 74 SMALL CHAIN.

PROPEP 75 94
CHAIN 95 175
CONFLICT 37 37 D -> N (IN REF. 4).

CONFLICT 76 76 S -> N (IN REF. 4).
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CONFLICT
SEQUENCE
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REVISIONS.
Josefsson |
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[3]
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PIR; A29801; A29801.
PIR; A25997; A25997.
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MEDLINE-87033665; PubMed-3771543;
Ericson M.L., Roedin J., Lenman M., Glimelius K., Josefsson L.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure of the rapeseed 1.7 S storage protein, napin, and its precursor.";
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[4]
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                                                                                                               28 ECREKYQENP 37
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S -> N (IN REF. 4).
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